

In the Claims:

1. (currently amended) A method, comprising:

- a) providing a biological sample from a subject, said biological sample comprising genomic DNA, ~~wherein said genomic DNA comprises a plurality of promoters from different genes;~~
- b) ~~digesting said genomic DNA in said biological sample with a methylation-sensitive restriction enzyme under conditions such that unmethylated CpG islands in said promoters are cleaved while methylated CpG islands in said promoters are not cleaved;~~
- c) ~~contacting said biological sample with gene specific primers, wherein said gene specific primers are configured to hybridize to said genomic DNA, and wherein said contacting is under conditions such that fragments of said plurality of promoters comprising uncleaved CpG islands are amplified, while cleaved promoters comprising cleaved CpG islands are not amplified; and~~
- bd) ~~detecting the presence or absence of DNA methylation in each of said plurality of promoters based on the amplification, or lack of amplification, of said fragments one or more genes to generate a methylation profile for said subject; and~~
- c) ~~comparing said methylation profile to one or more standard methylation profiles, wherein said standard methylation profiles are selected from the group consisting of methylation profiles of non-cancerous samples and methylation profiles of cancerous samples.~~

2. (currently amended) The method of Claim 1, wherein said ~~method further comprises comparing said methylation profile to more or more standard methylation profiles, wherein said standard methylation profiles are selected from the group consisting of methylation profiles of non-cancerous samples and methylation profiles of cancerous samples. detecting the presence or absence of DNA methylation comprises the digestion of said genomic DNA with a methylation-sensitive restriction enzyme followed by multiplexed amplification of gene-specific DNA fragments with CpG islands.~~

3. (currently amended) A method of characterizing cancer, comprising:
 - a) providing a biological sample from a subject diagnosed with breast cancer, said biological sample comprising genomic DNA; and
 - b) detecting the presence or absence of DNA methylation in each of DAPK, GSTP, p15, MDR1, Progesterone Receptor, Calcitonin, ~~RIZ~~ RIZ1, and RARbeta genes to generate a profile, thereby characterizing said breast cancer in said subject.
4. (currently amended) The method of claim 3, further comprising the step of detecting the presence or absence of DNA methylation in one or more genes selected from the group consisting of S100A2, SRBC, BRCA1, HIN1, Cyclin D2, TMS1, HIC-1, hMLH1, E-cadherin, 14-3-3sigma, and MDGI.
5. (original) The method of claim 3, wherein said characterizing cancer comprises detecting the presence or absence of chemotherapy resistant cancer.
6. (original) The method of claim 5, wherein said chemotherapy is a nonsteroidal selective estrogen receptor modulator.
7. (original) The method of claim 3, wherein said characterizing cancer comprises determining a chance of disease-free survival.
8. (original) The method of claim 3, wherein said characterizing cancer comprises determining the risk of developing metastatic disease.
9. (original) The method of claim 3, wherein said characterizing cancer comprises monitoring disease progression in said subject.
10. (original) The method of claim 3, wherein said biological sample is a biopsy sample.
11. (currently amended) The method of claim 3, wherein said biological sample is a blood plasma sample.

12. (original) The method of claim 3, wherein said DNA methylation comprises CpG methylation.

13. (original) The method of claim 3, wherein said detecting the presence or absence of DNA methylation comprises the digestion of said genomic DNA with a methylation-sensitive restriction enzyme followed by multiplexed amplification of gene-specific DNA fragments with CpG islands.

14. (original) The method of claim 13, wherein said methylation-sensitive restriction enzyme comprises Hin6I.

15. (cancelled)

16-20. (canceled)

21. (previously presented) The method of claim 1, wherein said biological sample is a biopsy sample.

22. (currently amended) The method of claim 1, wherein said biological sample is a blood plasma sample.

23. (previously presented) The method of claim 1, wherein said DNA methylation comprises CpG methylation.

24. (previously presented) The method of claim 1, wherein said cancer is breast cancer.

25. (new) The method of Claim 1, wherein said methylation-sensitive restriction enzyme comprises Hin 6I.

26. (new) The method of Claim 1, further comprising the step of i) separating said biological sample into a control sample and an experimental sample, and ii) adding control nucleic acid to both said control and experimental samples, wherein said control nucleic acid comprises at least one known CpG island that is unmethylated.

27. (new) The method of Claim 26, wherein said control sample is not exposed to said digesting and said experimental sample is exposed to said digesting, and wherein both said control and experimental samples are contacted with primers specific for said control nucleic acid under conditions such that a fragment of said control nucleic acid is amplified only if said known CpG island is uncleaved.

28. (new) The method of Claim 27, further comprising comparing any fragments amplified in said control and experimental samples to confirm that said digesting in step b) is complete.

29. (new) The method of Claim 1, wherein said plurality of different promoters comprises at least 5 different promoters from at least 5 different genes.

30. (new) The method of Claim 1, wherein said plurality of different promoters comprises at least 40 different promoters from at least 40 different genes.

31. (new) The method of Claim 1, wherein said digesting is performed to completion.

32. (new) A method of characterizing cancer, comprising:

- a) providing a biological sample from a subject diagnosed with breast cancer, said biological sample comprising genomic DNA; and
- b) detecting the presence or absence of DNA methylation in a group of genes, wherein said group of genes consists of: DAPK, GSTP, p15, MDR1, Progesterone Receptor, Calcitonin, RIZ1, and RARbeta genes to generate a profile, thereby characterizing said breast cancer in said subject.